



Universität für Bodenkultur Wien
University of Natural Resources
and Life Sciences, Vienna

Department für Chemie
Department of Chemistry



Measurement uncertainty in quantitative metabolomics

Teresa Mairinger^a, Stephan Hann^a, Wolfhard Wegscheider^b

^aDepartment of Chemistry, University of Natural Resources and Life Sciences – BOKU Vienna

^bDepartment of General, Analytical and Physical Chemistry, Montanuniversitaet Leoben

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Outline

- Biological and industrial relevance
- Metabolomics and measurements
- Concentrations and fluxes
- Alternative metabolic pathways
- Analytical approach
- Uncertainty of measurement and correction

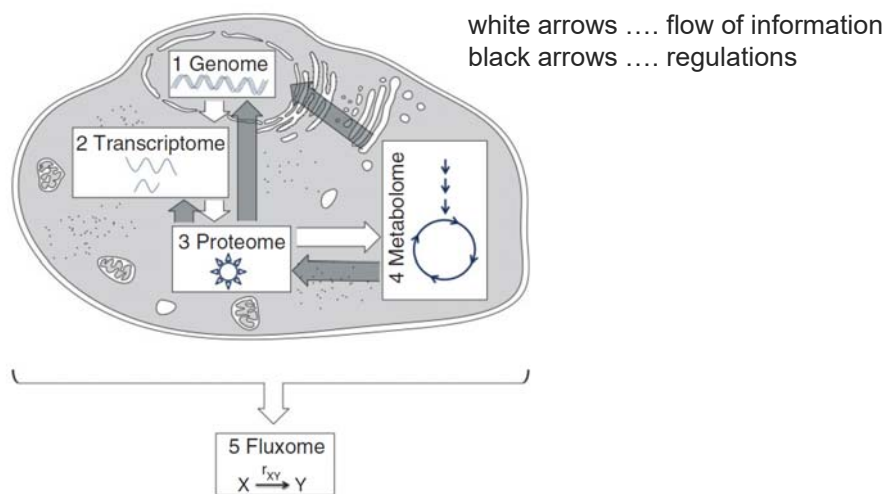
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Biochemical Studies of Living Cells

- Bacteria, fungi, mammalian, plant
- Understanding metabolism
- Understanding the interactions between compartments in cells
- Understanding the effect of extraneous chemicals (drugs, poisons) on the cell
- Producing chemicals, proteins and drugs from cell cultures
- Enhancing these production pathways

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Cell compartments and interactions



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S. Klein and E. Heinzle, 2012

Metabolomics

- Provides absolute or relative metabolite levels (intracellular or extracellular)
- BUT: Concentration changes cannot unambiguously be interpreted as changes of metabolic rates (fluxes)
- Increase in concentration can be from:
 - Increased activity of producing enzymes
 - Increased pool (reservoir) within cell
 - Decreased activity of consuming enzymes

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J. M. Buescher et al., 2015

The measurement problem

- Small quantities of cell mass (mg)
- Numerous small molecules involved in metabolic pathway
- Most of the molecules are highly reactive
- Temporary development of concentration profiles is relevant
- Difficult to „freeze“ the temporary state
- Temporary state inferred from degree of labelling of molecules via ^{13}C glucose

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Analytical solution

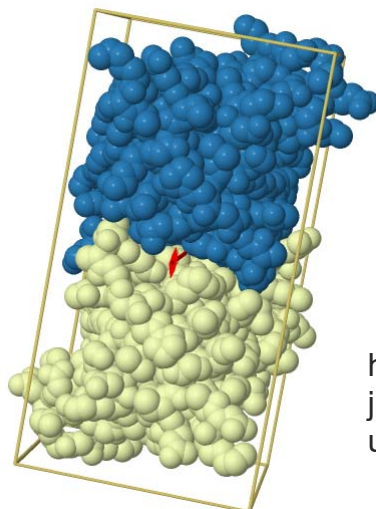
42 analytes in *Pichia pastoris* broth for production of human superoxide dismutase

- Quenching of metabolism: sampling of cell broth into 60% MeOH at -30° C
- Filtered and stored at -80° C
- Extracted with 4 ml EtOH (75%) for 3 min at 85° C
- Automated ethoximation and trimethylsilylation
- GC-CI-TOFMS

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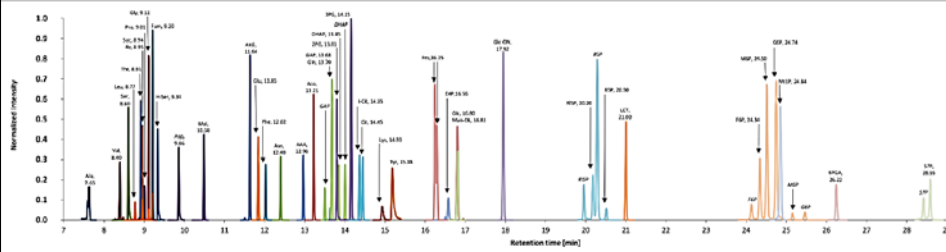
T. Mairinger et al., 2015

Human Cu-Zn superoxide dismutase mutant G93A



<http://www.rcsb.org/pdb/explore/jmol.do?structureId=2ZKY&biomumber=5&view=symmetry>

GC-run



- Amino acids
- Sugars
- Phosphates
- Intermediates

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T. Mairinger et al., 2015

Mass spectrometric pattern from isotopologues

- ^{13}C labelling for a C-3 molecule
 - Random statistical frequency 1:3:3:1

	raw labeling data	ion count (IC) <i>(freely chosen example)</i>	total ion count (TIC)	MDV (IC/TIC)
metabolite with three C atoms	○○○ M+0	10500	$\Sigma = 88000$	0.12
	○○● M+1	22000		0.25
	●●○ M+2	15000		0.17
	●●● M+3	40500		0.46

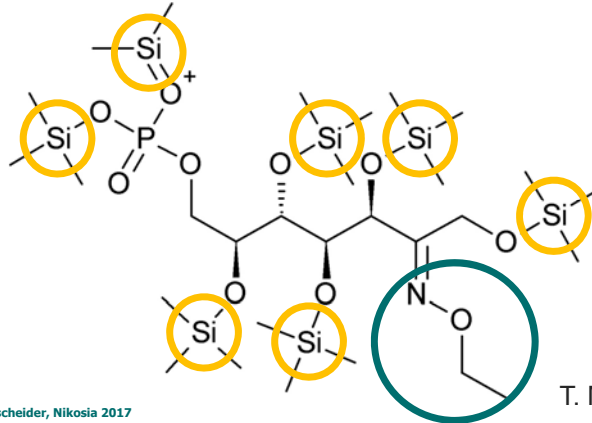
- The bigger the molecule the more isotopologues

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J.M. Buescher et al., 2015

One of 42 analytes: Sedoheptulose-7-phosphate

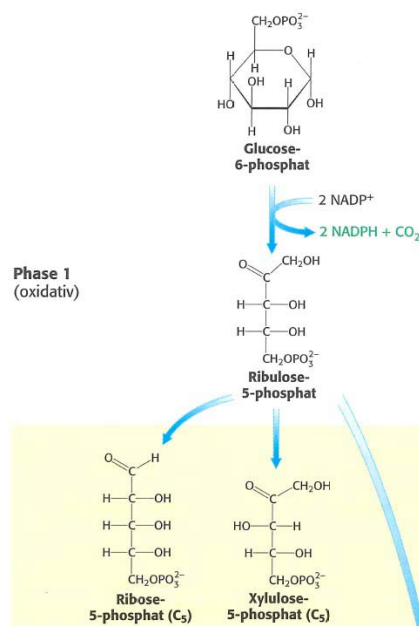
- 7 Trimethylsilyl and 1 Ethoximate
- 29 C atoms and 7 Si atoms



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T. Mairinger et al., 2015

20.3 • Der Pentosephosphatweg erzeugt NADH



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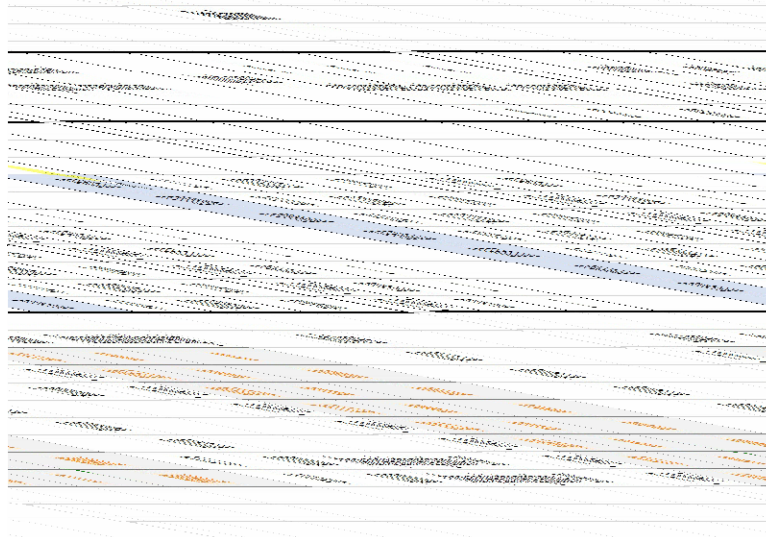
Stryer Biochemie, 2013

Components of uncertainty

- From analytical protocol:
 - Ionization and transmission efficiency
 - Poisson statistics
 - Background subtraction
 - Integration
- From naturally occurring isotopes:
 - ^{13}C in backbone and derivatization reagent
 - ^{28}Si , ^{29}Si , ^{30}Si in derivatization reagent

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Excel solution for analytical protocol



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Excel solution for naturally occurring isotopes

Data from:

	counting statistics	peak integration	ionization and transmission	Input areas	IF not corrected %	IF not corrected SD	IF not corrected RSD
IF_M	3659	1	1	3659	2.1	0,03729	1,7%
IF_M+1	52784	1		52784	31,0	0,2246	0,7%
IF_M+2	51881	1		51881	30,4	0,2228	0,7%
IF_M+3	35625	1		35625	20,9	0,1797	0,9%
IF_M+4	16555	1		16555	9,7	0,10417	1,1%
IF_M+5	6813	1		6813	4,0	0,05589	1,4%
IF_M+6	2385	1		2385	1,4	0,03109	2,2%
IF_M+7	738	1		738	0,4	0,01638	3,8%

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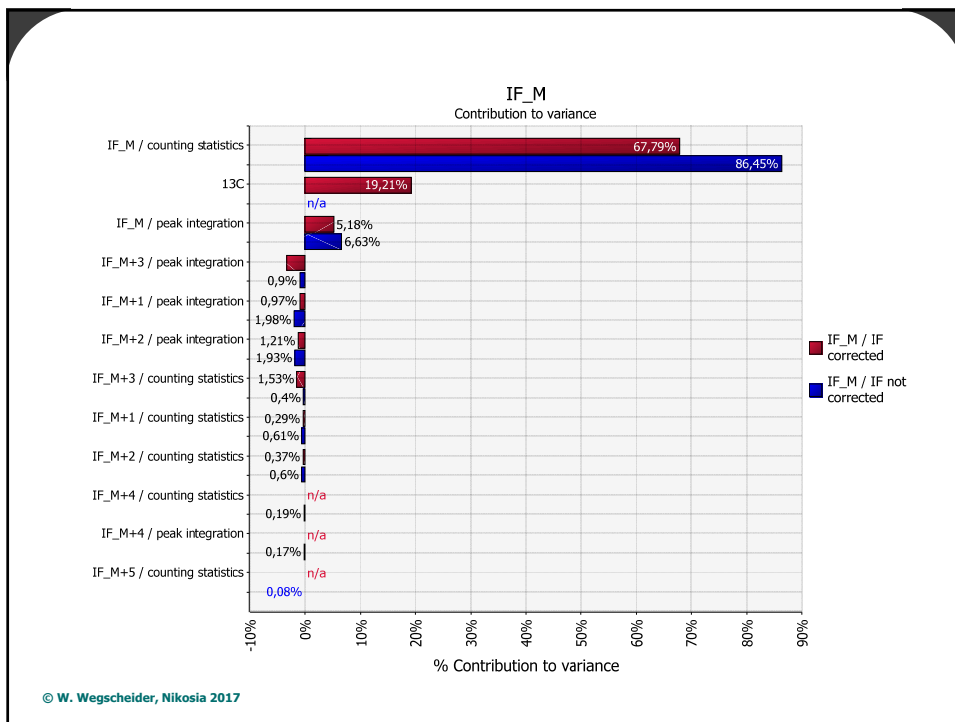
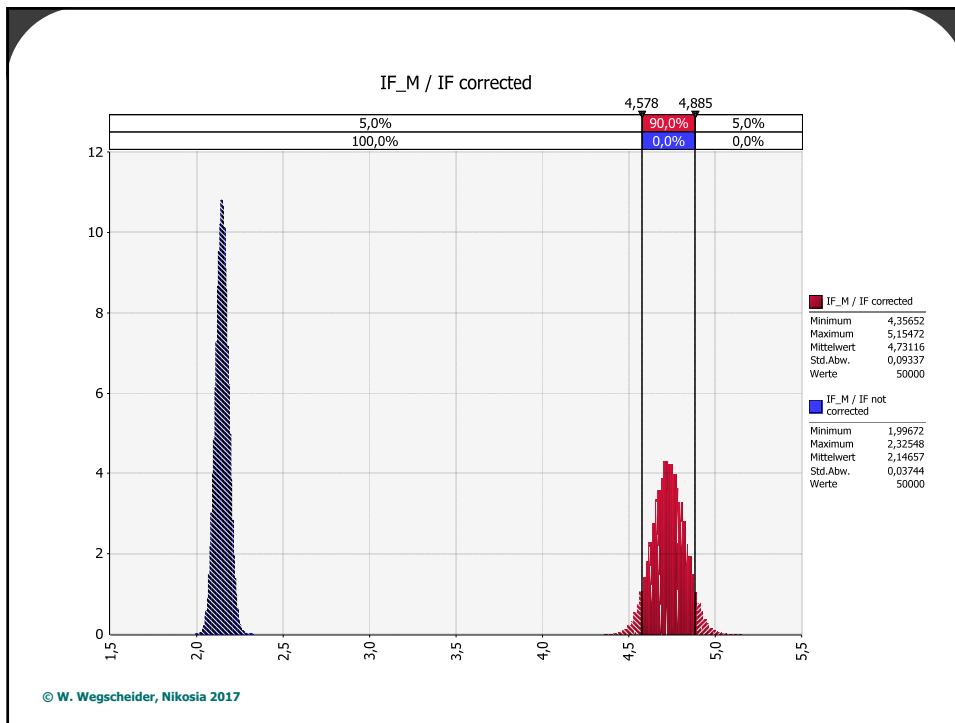
Monte Carlo Simulation

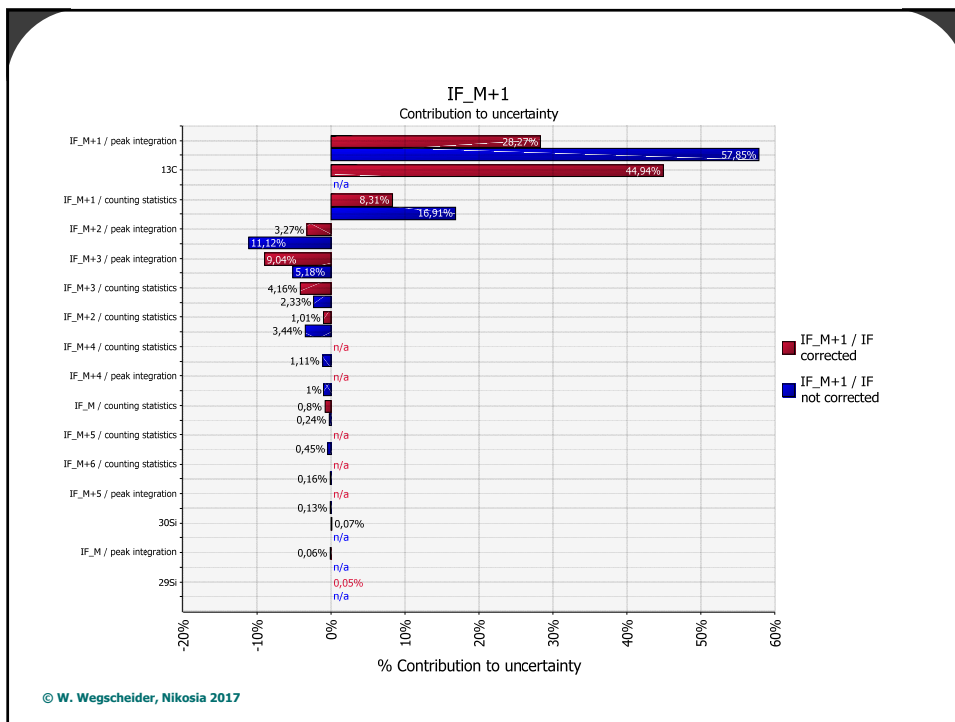
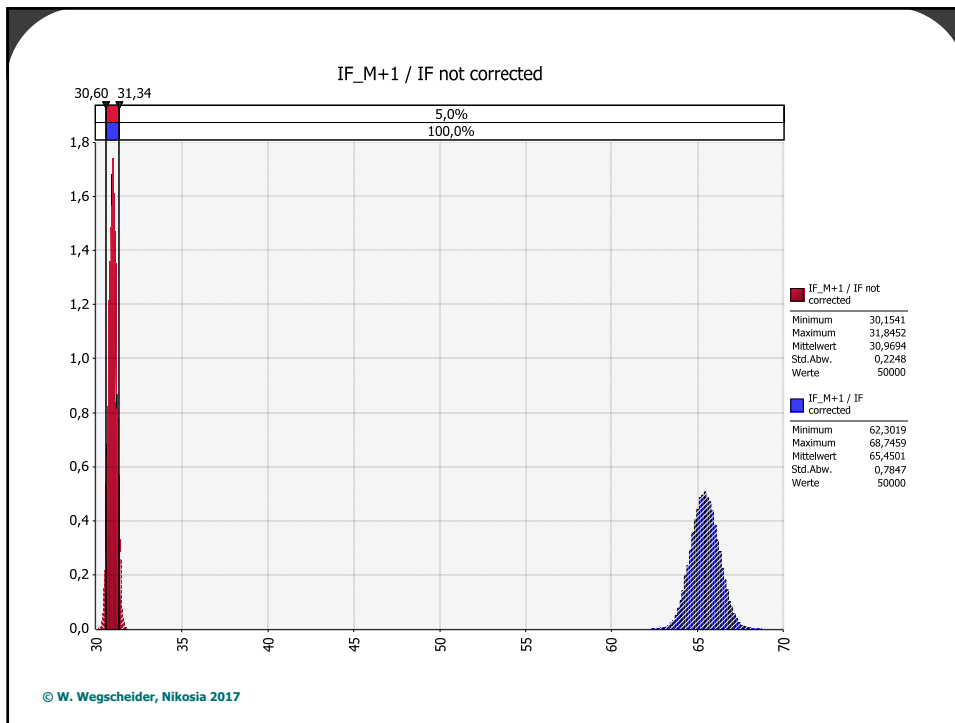
	Precursor	Fragment	Natural abundances	Normalized natural abundances
Sum formula derivate	C2957	C2957	3090 0,03092 13C 0,0107 345 0,04210	3090 0,03353 (va) 13C 0,01082 (vc) 345 0,04431 (vd)
Sum formula backbone	C7	C7	2950 0,04685 13C 0,9893 326 0,95020	2950 0,05080 (vb) 13C 1,00000 326 1,00000
Sum formula added groups			2950 0,92223	2950 1,00000

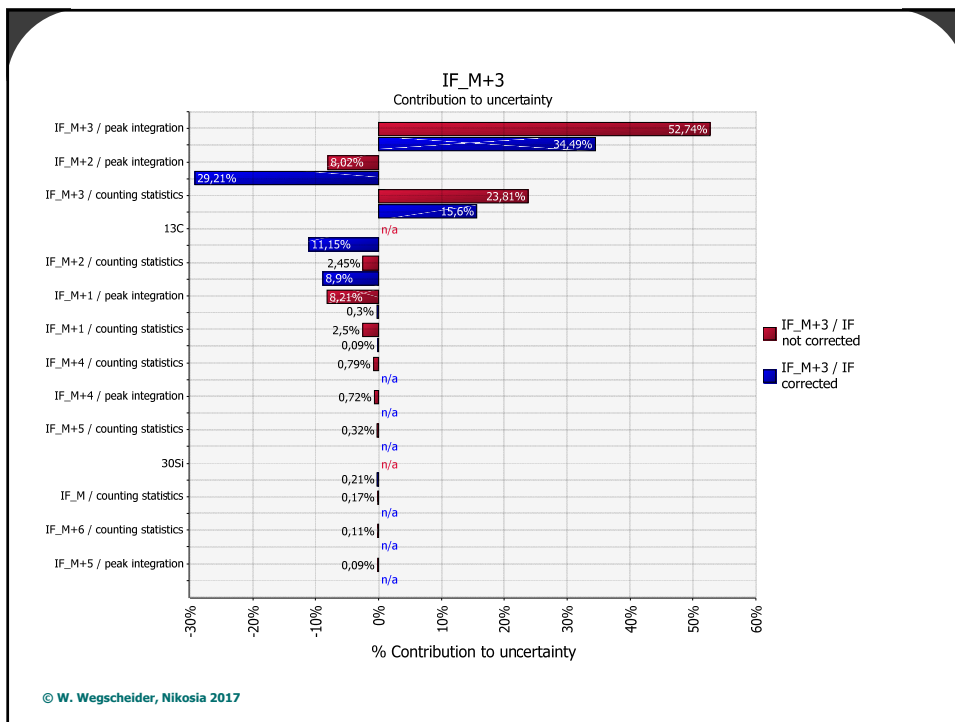
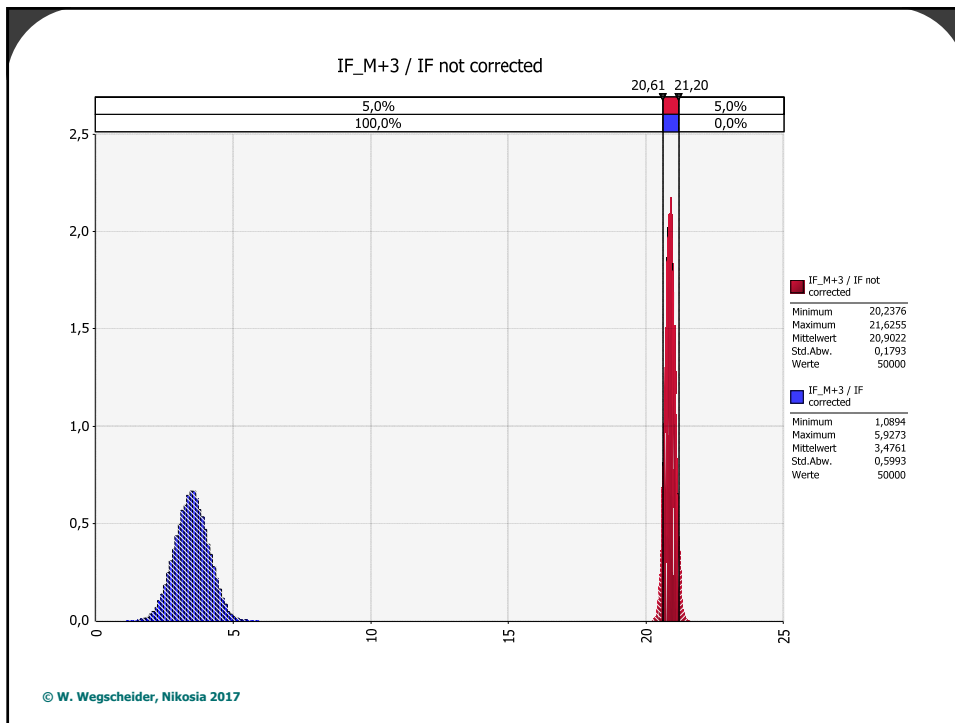
	m=0	m=1	m=2	m=3	m=4	m=5	m=6	m=7
m=0	x							
m=1	x							
m=2		x						
m=3			x					
m=4				x				
m=5					x			
m=6						x		
m=7							x	

	a'	b'
	0,000000000476213	0,0000000008731572
	0,00000000000476213	0,000000000008731572
	3090 3090 2950 2950 345 345 13C 13C 13C 13C	3090 3090 2950 2950 345 345 13C 13C 13C 13C
	7 7 0 0 0 0 0 0 0 0 14 14	0 0 7 7 0 0 0 0 0 0 0 7 7
	7 7 0 0 0 0 0 0 0 1 1 15 15	0 0 7 7 0 0 0 0 0 1 1 8 8
	7 7 0 0 0 0 0 0 0 2 2 16 16	0 0 7 7 0 0 0 0 0 2 2 9 9
	7 7 0 0 0 0 0 0 0 3 3 17 17	0 0 7 7 0 0 0 0 0 3 3 10 10

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Results for Sedoheptulose Phosphate

mass	IF uncorr	u(IF uncorr)	IF corr	u(IF corr)
IF_M	2,1	0,04	4,7	0,09
IF_M+1	31,0	0,23	65,4	0,78
IF_M+2	30,4	0,22	26,3	0,79
IF_M+3	20,9	0,18	3,5	0,60
IF_M+4	9,7	0,10	-1,7	0,35
IF_M+5	4,0	0,06	-0,7	0,22
IF_M+6	1,4	0,03	-0,2	0,10
IF_M+7	0,4	0,02	0,0	0,05

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Conclusions

- The analytical protocol can be considered fairly robust
- The corrections lead to significantly different „true“ isotopic signature from labelling
- The corrections for natural isotopic abundances cause an increase of uncertainty of about a factor of 3 - 4
- The significance of these corrections on the flux modelling is not yet established

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